

SEQUENCE LISTING

<110> Katherine Galvin and Laura A. Rudolph-Owen

<120> METHODS AND COMPOSITIONS FOR THE DIAGNOSIS
AND TREATMENT OF CARDIOVASCULAR AND TUMORIGENIC
DISEASE USING 4941

<130> MPI99-283P1RCN1M

<140>

<141>

<150> 09/635,521

<151> 2000-08-09

<150> 60/199,908

<151> 2000-04-26

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1359)

<400> 1

atg gct tca ccc agc ctc ccg ggc agt gac tgc tcc caa atc att gat	48
Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp	
1 5 10 15	
cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc	96
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr	
20 25 30	
ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac	144
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn	
35 40 45	
agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg	192
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu	
50 55 60	
cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc	240
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile	
65 70 75 80	
ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg	288
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp	
85 90 95	
aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act	336
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr	
100 105 110	
ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca	384

Phe	Leu	Phe	Glu	Ala	Cys	Ser	Tyr	Ala	Thr	Leu	Leu	His	Val	Leu	Thr		
		115					120					125					
ctc	agc	ttt	gag	cgc	tac	atc	gcc	atc	tgt	cac	ccc	ttc	agg	tac	aag	432	
Leu	Ser	Phe	Glu	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Phe	Arg	Tyr	Lys		
		130				135					140						
gct	gtg	tcg	gga	cct	tgc	cag	gtg	aag	ctg	ctg	att	ggc	ttc	gtc	tgg	480	
Ala	Val	Ser	Gly	Pro	Cys	Gln	Val	Lys	Leu	Leu	Ile	Gly	Phe	Val	Trp		
		145			150					155					160		
gtc	acc	tcc	gcc	ctg	gtg	gca	ctg	ccc	ttg	ctg	ttt	gcc	atg	ggg	act	528	
Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Thr		
				165				170						175			
gag	tac	ccc	ctg	gtg	aac	gtg	ccc	agc	cac	cgg	ggg	ctc	act	tgc	aac	576	
Glu	Tyr	Pro	Leu	Val	Asn	Val	Pro	Ser	His	Arg	Gly	Leu	Thr	Cys	Asn		
			180					185					190				
cgc	tcc	agc	acc	cgc	cac	cac	gag	cag	ccc	gag	acc	tcc	aac	atg	tcc	624	
Arg	Ser	Ser	Thr	Arg	His	His	Glu	Gln	Pro	Glu	Thr	Ser	Asn	Met	Ser		
		195					200					205					
atc	tgt	acc	aac	ctc	tcc	agc	cgc	tgg	acc	gtg	ttc	cag	tcc	agc	atc	672	
Ile	Cys	Thr	Asn	Leu	Ser	Ser	Arg	Trp	Thr	Val	Phe	Gln	Ser	Ser	Ile		
	210					215					220						
ttc	ggc	gcc	ttc	gtg	gtc	tac	ctc	gtg	gtc	ctg	ctc	tcc	gta	gcc	ttc	720	
Phe	Gly	Ala	Phe	Val	Val	Tyr	Leu	Val	Val	Leu	Leu	Ser	Val	Ala	Phe		
	225			230				235						240			
atg	tgc	tgg	aac	atg	atg	cag	gtg	ctc	atg	aaa	agc	cag	aag	ggc	tcg	768	
Met	Cys	Trp	Asn	Met	Met	Gln	Val	Leu	Met	Lys	Ser	Gln	Lys	Gly	Ser		
			245					250						255			
ctg	gcc	ggg	ggc	acg	cgg	cct	ccg	cag	ctg	agg	aag	tcc	gag	agc	gaa	816	
Leu	Ala	Gly	Gly	Thr	Arg	Pro	Pro	Gln	Leu	Arg	Lys	Ser	Glu	Ser	Glu		
			260					265					270				
gag	agc	agg	acc	gcc	agg	agg	cag	acc	atc	atc	ttc	ctg	agg	ctg	att	864	
Glu	Ser	Arg	Thr	Ala	Arg	Arg	Gln	Thr	Ile	Ile	Phe	Leu	Arg	Leu	Ile		
		275					280					285					
gtt	gtg	aca	ttg	gcc	gta	tgc	tgg	atg	ccc	aac	cag	att	cgg	agg	atc	912	
Val	Val	Thr	Leu	Ala	Val	Cys	Trp	Met	Pro	Asn	Gln	Ile	Arg	Arg	Ile		
	290					295					300						
atg	gct	gcg	gcc	aaa	ccc	aag	cac	gac	tgg	acg	agg	tcc	tac	ttc	cgg	960	
Met	Ala	Ala	Ala	Lys	Pro	Lys	His	Asp	Trp	Thr	Arg	Ser	Tyr	Phe	Arg		
	305				310					315				320			
gcg	tac	atg	atc	ctc	ctc	ccc	ttc	tcg	gag	acg	ttt	ttc	tac	ctc	agc	1008	
Ala	Tyr	Met	Ile	Leu	Leu	Pro	Phe	Ser	Glu	Thr	Phe	Phe	Tyr	Leu	Ser		
				325					330					335			
tcg	gtc	atc	aac	ccg	ctc	ctg	tac	acg	gtg	tcc	tcg	cag	cag	ttt	cgg	1056	
Ser	Val	Ile	Asn	Pro	Leu	Leu	Tyr	Thr	Val	Ser	Ser	Gln	Gln	Phe	Arg		
			340				345						350				
cgg	gtg	ttc	gtg	cag	gtg	ctg	tgc	tgc	cgc	ctg	tcg	ctg	cag	cac	gcc	1104	
Arg	Val	Phe	Val	Gln	Val	Leu	Cys	Cys	Arg	Leu	Ser	Leu	Gln	His	Ala		
		355					360						365				

aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc	1152
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser	
370 375 380	
gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc	1200
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser	
385 390 395 400	
tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag	1248
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu	
405 410 415	
gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag	1296
Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu	
420 425 430	
ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt	1344
Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe	
435 440 445	
cag gag cat gaa gtt tga	1362
Gln Glu His Glu Val	
450	
<210> 2	
<211> 453	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp	
1 5 10 15	
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr	
20 25 30	
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn	
35 40 45	
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu	
50 55 60	
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile	
65 70 75 80	
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp	
85 90 95	
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr	
100 105 110	
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr	
115 120 125	
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys	
130 135 140	
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp	
145 150 155 160	

Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Thr		
				165					170					175			
Glu	Tyr	Pro	Leu	Val	Asn	Val	Pro	Ser	His	Arg	Gly	Leu	Thr	Cys	Asn		
			180					185					190				
Arg	Ser	Ser	Thr	Arg	His	His	Glu	Gln	Pro	Glu	Thr	Ser	Asn	Met	Ser		
		195					200					205					
Ile	Cys	Thr	Asn	Leu	Ser	Ser	Arg	Trp	Thr	Val	Phe	Gln	Ser	Ser	Ile		
	210					215					220						
Phe	Gly	Ala	Phe	Val	Val	Tyr	Leu	Val	Val	Leu	Leu	Ser	Val	Ala	Phe		
225				230						235					240		
Met	Cys	Trp	Asn	Met	Met	Gln	Val	Leu	Met	Lys	Ser	Gln	Lys	Gly	Ser		
			245						250					255			
Leu	Ala	Gly	Gly	Thr	Arg	Pro	Pro	Gln	Leu	Arg	Lys	Ser	Glu	Ser	Glu		
			260					265					270				
Glu	Ser	Arg	Thr	Ala	Arg	Arg	Gln	Thr	Ile	Ile	Phe	Leu	Arg	Leu	Ile		
		275					280					285					
Val	Val	Thr	Leu	Ala	Val	Cys	Trp	Met	Pro	Asn	Gln	Ile	Arg	Arg	Ile		
	290					295					300						
Met	Ala	Ala	Ala	Lys	Pro	Lys	His	Asp	Trp	Thr	Arg	Ser	Tyr	Phe	Arg		
305					310					315					320		
Ala	Tyr	Met	Ile	Leu	Leu	Pro	Phe	Ser	Glu	Thr	Phe	Phe	Tyr	Leu	Ser		
			325						330					335			
Ser	Val	Ile	Asn	Pro	Leu	Leu	Tyr	Thr	Val	Ser	Ser	Gln	Gln	Phe	Arg		
			340					345					350				
Arg	Val	Phe	Val	Gln	Val	Leu	Cys	Cys	Arg	Leu	Ser	Leu	Gln	His	Ala		
		355					360					365					
Asn	His	Glu	Lys	Arg	Leu	Arg	Val	His	Ala	His	Ser	Thr	Thr	Asp	Ser		
	370					375					380						
Ala	Arg	Phe	Val	Gln	Arg	Pro	Leu	Leu	Phe	Ala	Ser	Arg	Arg	Gln	Ser		
385				390						395					400		
Ser	Ala	Arg	Arg	Thr	Glu	Lys	Ile	Phe	Leu	Ser	Thr	Phe	Gln	Ser	Glu		
			405					410						415			
Ala	Glu	Pro	Gln	Ser	Lys	Ser	Gln	Ser	Leu	Ser	Leu	Glu	Ser	Leu	Glu		
			420					425					430				
Pro	Asn	Ser	Gly	Ala	Lys	Pro	Ala	Asn	Ser	Ala	Ala	Glu	Asn	Gly	Phe		
	435						440					445					
Gln	Glu	His	Glu	Val													
	450																

<210> 3

<211> 2528

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (42)..(1400)

<220>
 <223> N at positions 2490 and 2493 may be Adenine,
 Guanine, Cytosine or Thymine

<400> 3

gggagtcgac ccacgcgtcc ggtagcctgg tgctctttct c atg gct tca ccc agc 56
 Met Ala Ser Pro Ser
 1 5

ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc 104
 Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro
 10 15 20

gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac 152
 Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr
 25 30 35

ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg 200
 Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg
 40 45 50

gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca 248
 Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr
 55 60 65

gac cac atg gtg agt ttg gct tgc tcg gac atc ttg gtg ttc ctc atc 296
 Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile
 70 75 80 85

ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg 344
 Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr
 90 95 100

tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc 392
 Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala
 105 110 115

tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc 440
 Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg
 120 125 130

tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct 488
 Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro
 135 140 145

tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg 536
 Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu
 150 155 160 165

gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg 584
 Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val
 170 175 180

aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc 632
 Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg
 185 190 195

cac	cac	gag	cag	ccc	gag	acc	tcc	aat	atg	tcc	atc	tgt	acc	aac	ctc	680
His	His	Glu	Gln	Pro	Glu	Thr	Ser	Asn	Met	Ser	Ile	Cys	Thr	Asn	Leu	
		200					205					210				
tcc	agc	cgc	tgg	acc	gtg	ttc	cag	tcc	agc	atc	ttc	ggc	gcc	ttc	gtg	728
Ser	Ser	Arg	Trp	Thr	Val	Phe	Gln	Ser	Ser	Ile	Phe	Gly	Ala	Phe	Val	
	215					220					225					
gtc	tac	ctc	gtg	gtc	ctg	ctc	tcc	gta	gcc	ttc	atg	tgc	tgg	aac	atg	776
Val	Tyr	Leu	Val	Val	Leu	Leu	Ser	Val	Ala	Phe	Met	Cys	Trp	Asn	Met	
230					235				240						245	
atg	cag	gtg	ctc	atg	aaa	agc	cag	aag	ggc	tgc	ctg	gcc	ggg	ggc	acg	824
Met	Gln	Val	Leu	Met	Lys	Ser	Gln	Lys	Gly	Ser	Leu	Ala	Gly	Gly	Thr	
				250					255					260		
cgg	cct	ccg	cag	ctg	agg	aag	tcc	gag	agc	gaa	gag	agc	agg	acc	gcc	872
Arg	Pro	Pro	Gln	Leu	Arg	Lys	Ser	Glu	Ser	Glu	Glu	Ser	Arg	Thr	Ala	
			265					270					275			
agg	agg	cag	acc	atc	atc	ttc	ctg	agg	ctg	att	gtt	gtg	aca	ttg	gcc	920
Arg	Arg	Gln	Thr	Ile	Ile	Phe	Leu	Arg	Leu	Ile	Val	Val	Thr	Leu	Ala	
		280					285				290					
gta	tgc	tgg	atg	ccc	aac	cag	att	cgg	agg	atc	atg	gct	gcg	gcc	aaa	968
Val	Cys	Trp	Met	Pro	Asn	Gln	Ile	Arg	Arg	Ile	Met	Ala	Ala	Ala	Lys	
	295					300					305					
ccc	aag	cac	gac	tgg	acg	agg	tcc	tac	ttc	cgg	gcg	tac	atg	atc	ctc	1016
Pro	Lys	His	Asp	Trp	Thr	Arg	Ser	Tyr	Phe	Arg	Ala	Tyr	Met	Ile	Leu	
310					315					320					325	
ctc	ccc	ttc	tgc	gag	acg	ttt	ttc	tac	ctc	agc	tgc	gtc	atc	aac	ccg	1064
Leu	Pro	Phe	Ser	Glu	Thr	Phe	Phe	Tyr	Leu	Ser	Ser	Val	Ile	Asn	Pro	
				330				335						340		
ctc	ctg	tac	acg	gtg	tcc	tgc	cag	cag	ttt	cgg	cgg	gtg	ttc	gtg	cag	1112
Leu	Leu	Tyr	Thr	Val	Ser	Ser	Gln	Gln	Phe	Arg	Arg	Val	Phe	Val	Gln	
			345				350					355				
gtg	ctg	tgc	tgc	cgc	ctg	tgc	ctg	cag	cac	gcc	aac	cac	gag	aag	cgc	1160
Val	Leu	Cys	Cys	Arg	Leu	Ser	Leu	Gln	His	Ala	Asn	His	Glu	Lys	Arg	
		360				365					370					
ctg	cgc	gta	cat	gcg	cac	tcc	acc	acc	gac	agc	gcc	cgc	ttt	gtg	cag	1208
Leu	Arg	Val	His	Ala	His	Ser	Thr	Thr	Asp	Ser	Ala	Arg	Phe	Val	Gln	
	375					380					385					
cgc	ccg	ttg	ctc	ttc	gcg	tcc	cgg	cgc	cag	tcc	tct	gca	agg	aga	act	1256
Arg	Pro	Leu	Leu	Phe	Ala	Ser	Arg	Arg	Gln	Ser	Ser	Ala	Arg	Arg	Thr	
390				395					400						405	
gag	aag	att	ttc	tta	agc	act	ttt	cag	agc	gag	gcc	gag	ccc	cag	tct	1304
Glu	Lys	Ile	Phe	Leu	Ser	Thr	Phe	Gln	Ser	Glu	Ala	Glu	Pro	Gln	Ser	
			410				415							420		
aag	tcc	cag	tca	ttg	agt	ctc	gag	tca	cta	gag	ccc	aac	tca	ggc	gcg	1352
Lys	Ser	Gln	Ser	Leu	Ser	Leu	Glu	Ser	Leu	Glu	Pro	Asn	Ser	Gly	Ala	
			425				430						435			
aaa	cca	gcc	aat	tct	gct	gca	gag	aat	ggc	ttt	cag	gag	cat	gaa	gtt	1400
Lys	Pro	Ala	Asn	Ser	Ala	Ala	Glu	Asn	Gly	Phe	Gln	Glu	His	Glu	Val	

440

445

450

tgaatgtcaa gcgaggggagc cttgagtggg aactggccct ccagccctaa gaaaacgtca 1460
 ctctcactct gcagtctcaa actatgcccc catcagggat ggaatggaca ctggaggctt 1520
 tacaaaaggc agatgcccac ctcaagtact tctaaggact gactctgcca gcctggcctt 1580
 gactccggtt acacagacat ggggggtgaac tttcactcca cctccttctt tcaagtacat 1640
 actgaaaatt cagtcaagct gaattttattc agaatgcttt accgagctct ttcattattt 1700
 gcacaggaac aaaagagAAC acggactccc gctccctacc cagaataaaa ggacacccag 1760
 aagaaactca ctcaggaggg tgggggggttg ggggcgaggg ctggaagaac aatgcaggag 1820
 ggggtggcat ctcttcagc ttcagcagtg tgccgagaag agggctaatt tgaggaacag 1880
 gatggtggtg cggagccctg gcctgagggc cgaggcagaa cttccccttt tcttgggcct 1940
 tggcccgtta caaagagggg tgttgagca gctgatgcaa actgagttca gtttccctgg 2000
 ggagcagaag gactggtacc cggcagaggc gatgagacag gccgctgatg atgcacagga 2060
 cttgcggtac atgatcccg cactttgctc catcacttct ttctgacaca tgtcttgaac 2120
 gttcacctg caattcaca tgaactcggg ggaggagcag tcgttggttca gctggaattc 2180
 ttcacactgg tagcactgga tttgcagcgc aaagccttgc ggactcccgg ggatgccccg 2240
 gtgctatctt cgccttcctt cccgagcctt gcagcaggtg gtgcgggaga ccgcttgccc 2300
 gccggagtgc gttggtgccc ccgcccccaa tccgcacatt cccatcccct ttccgcacat 2360
 ccttagggag catccatttc cgtggaaatc gcctcctaag ctttagctcc tcttcaccct 2420
 ttttcccccc ggccatttct gggggcagct ctctcacgcc gggacgcaga tcatttaatt 2480
 ctgcatcgcn tcngcagagc tgggtctgtaa aggggcttaa atgacttt 2528